



In 129 and

Q506 clumps

~~(F)~~

~~to  $A_n \in (k)$~~

~~This mutation~~

was found in

F-clone only.

~~bat~~ bat occur

in both 129 and

Q508 mutant

Lives

Again, they

~~region was~~

~~confident from~~

**DATE**

DATE \_\_\_\_\_

## EXPERIMENTER

RELEASED BY

TITLE

cont'd

DATE

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PURPOSE

cont'd

Book No.

E 79066

425 630 635 640 645 650 655 660 665 670  
TGC CAT TTC CAC CEC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC  
ACG GTA AAG GTG GGG TTG CGA GGG TAG ATG TTG CTG GCG CTC GCA GAG  
C H F H P N A P I Y N D R E R L>  
675 680 685 690 695 700 705 710 715 720  
CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCG GTC TCC TAC GGT CTC  
GTC TAT ATG TAG AGG CTG CGA CCG TAG GAG CCG CAG ACC ATG CCA GAG  
Q I Y I S D A G I L A V C Y G L>  
725 730 735 740 745 750 755 760 765  
TAC CGC TAC GCT GCT GTC CAA GGA GTT GCC TCG ATG GTC TCC TTC TAC  
ATG CCG ATG CGA CGA CAG GTT CCT CAA CCG AGC TAC CAG ACG AAG ATG  
Y R Y A A A V Q G V A S M V C F Y>  
770 775 780 785 790 795 800 805 810 815  
GGA GTT CCG CTT CTC ATT GTC AAT GCG TTC TTA GTT TTG ATC ACT TAC  
CCT CAA GGC GAA GAC TAA CAG TTA CCG AAG AAT CAA AAC TAG TGA ATG  
G V P L L I V N G F L V L I T Y>  
820 825 830 835 840 845 850 855 860  
TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCG TCT GAG TGG  
AAC GTC GTG TGC GTA GGA AGG GAC GGA GTC ATA CTG AGC AGA CTC ACC  
L Q H T H P S L P H Y D S S E W>  
865 870 875 880 885 890 895 900 905 910  
CAT TGG TTG AGG GGA GCT TTG GCC ACC GTT GAC AGA GAC TAC GGA ATC  
CTA ACC AAC TCC CCT CGA AAC CCG TCG CAA CTG TCT CTG ATG CCT TAG  
D W L R G A L A T V D R D Y G I>  
915 920 925 930 935 940 945 950 955 960  
TTG AAC AAG GTC TTC CAC AAT ATC ACG GAC ACG CAC GTG GCG CAT CAC  
AAC TTG TTC CAG AAG GTG TTA TAC TGC CTG TGC GTC CAC CCG GTA GTG  
L N K V F H N I T D T H V A H N>  
965 970 975 980 985 990 995 1000 1005  
CTG TTC TCG ACC ATG CCG CAT TAT CAT CCG ATC GAA GCT ACG AAG CCG  
GAC AAG AGC TGG TAC GGC GTA ATA GTA CCG TAC CTT CGA TGC TTC CCG  
L F S T M P H Y N A M E A T K A>  
1010 1015 1020 1025 1030 1035 1040 1045 1050 1055  
ATA AAG CCG ATA CTC GGA GAG TAT TAT CAG TTG CAT GGG ACG CCG GTG  
TAT TTC GGC TAT GAC CCT CTC ATA ATA GTC AAC GTA CCC TGC GCG CAC  
I K P I L G E Y Q L H G T P V>  
1060 1065 1070 1075 1080 1085 1090 1095 1100  
GTT AAG CCG ATG TGG AGG GAG CCG AAC GAG TGT ATC TAT CTG GAA CCG  
CAA TTC CCG TAC ACC TGC CTC CCG TTC CTC ACA TAG ATA CAC CTT GCG  
V K A M W R E A K E C I Y V E P>  
1105 1110 1115 1120 1125 1130 1135 1140 1145 1150  
GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA  
CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT  
D R Q G E K K G V F W Y N N H L>  
1155 1160 1165 1170  
TGA AGC AAA GAA GAA ACA AT  
ACT TCG TTT CTT CTT TGT TA  
S K E E T X>

Wala strand

(see pgs 134)

for primer location

Total 5 indels

12 and 9508

Chas (each with

ins) were

sequenced by

primer DR

(see pgs 134)

and showed the

same mutation

Thus it appears

to be true

mutation

This will be

further confirmed

by 12 RT-PCR

RNA from 12 cells

and sequenced by

DR primer

DATE